05 - Checking Normality, Transformations to Near Normality

Junvie Pailden

SIUE, F2017, Stat 589

September 04, 2017

Investigating Univariate Normality

- Could check each of the p variables for normality. Should not be the sole approach because variables are correlated and normality of individual variables does not guarantee multivariate normality.
- However, multivariate normality implies individual normality. Thus, if one of the variables is not univariate normal, then the vector is not multivariate normal.
- One check Q-Q (Quantile-Quantile) plot or normal probability plot for each variable. If normal, then the Q-Q plot is a straight line - subjective.

Constructing Q-Q plots

- Order the original observations to get $x_{(1)}, x_{(2)}, \ldots, x_{(n)}$ and their corresponding probability values $(1 - \frac{1}{2})/n, (2 - \frac{1}{2})/n, \ldots, (n - \frac{1}{2})/n$;

- Calculate the standard normal quantiles $q_{(1)}, q_{(2)}, \ldots, q_{(n)}$; and

- Plot the pairs of observations $(q_{(1)}, x_{(1)}), (q_{(2)}, x_{(2)}), \ldots, (q_{(n)}, x_{(n)})$, and examine the "straightness" of the outcome.

Investigating Bivariate Normality

- Check the scatter plot of each pair of the p variables.
- The points on each scatter plot should form approximately an ellipse since the contours of Bivariate Normal Distributions are ellipses.
- The set of generalized distances from each point to the center of the points is chi-square - Check using a chi-square plot.

Example: Reaven and Miller (1979)

Reaven and Miller measured five variables in a comparison of normal patients and diabetics. We use partial data for normal patients only. The three variables of major interest were

- X_1= glucose intolerance,
- X_2 = insulin response to oral glucose,
- X_3= insulin resistance.

The two additional variables of minor interest were
* Y_1 = relative weight,
* Y_2 = fasting plasma glucose.

```r
# load data set
patients <- read.csv("patients.csv", header = TRUE)
str(patients) # structure
```

```
# 'data.frame': 46 obs. of  5 variables:
#  $ WEIGHT : num  0.81 0.95 0.94 1.04 1 0.76 0.91 1.1 0.99
#  $ FASTING: int  80 97 105 90 90 86 100 85 97 97 ...
#  $ GLUCOSE: int  356 289 319 356 323 381 350 301 379 296
#  $ INSULIN: int  124 117 143 199 240 157 221 186 142 131
#  $ RESIST : int  55 76 105 108 143 165 119 105 98 94 ...
```

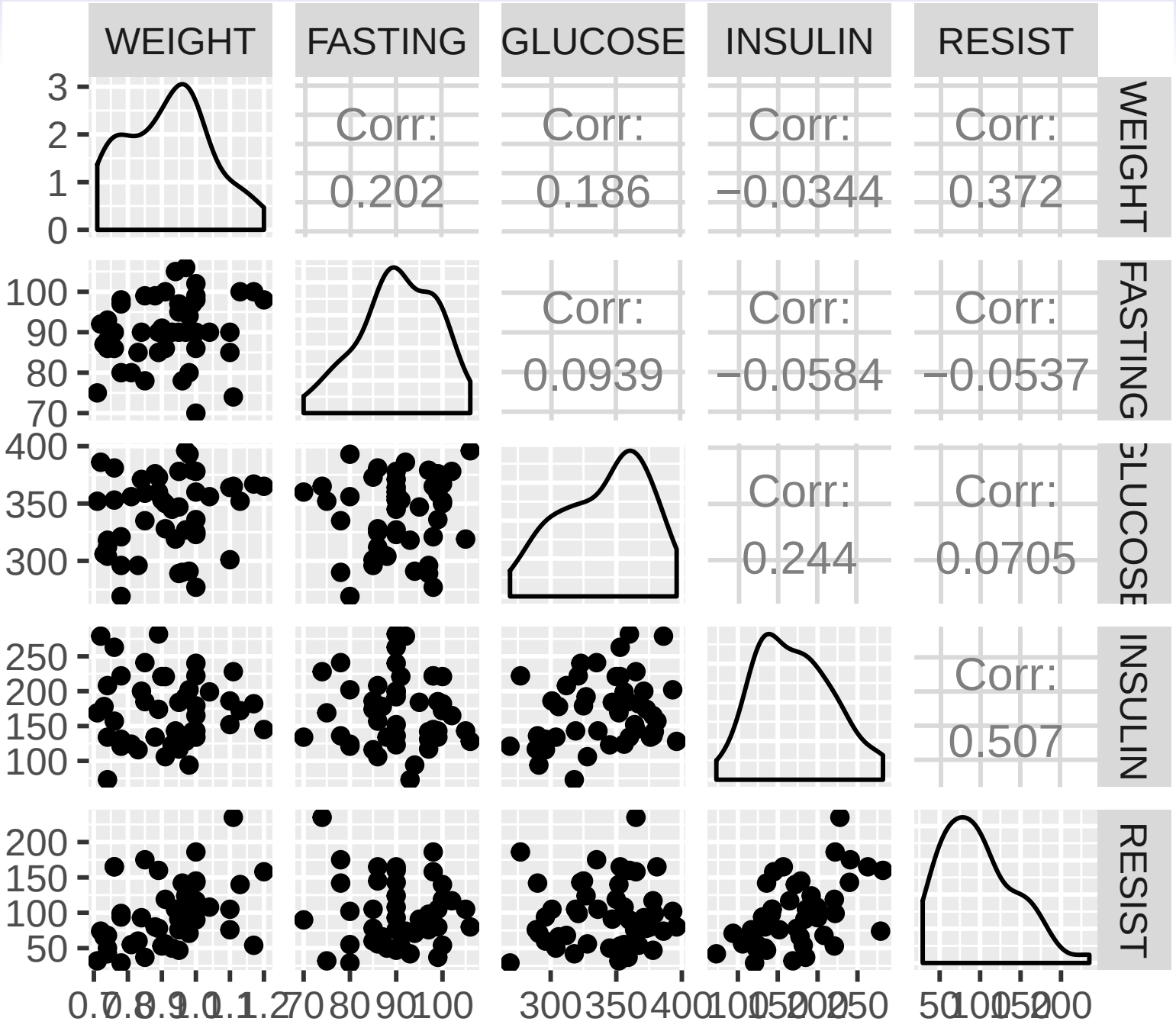
Descriptive Summary Statistics

```
data.frame(Mean = colMeans(patients),
           Median = apply(patients, 2, median),
           Variance = apply(patients, 2, var))
```

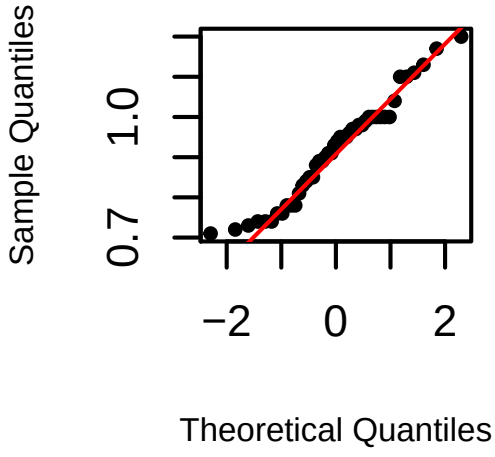
```
#             Mean Median Variance
# WEIGHT      0.92   0.94  1.6e-02
# FASTING    90.41  90.00  7.1e+01
# GLUCOSE   340.83 351.00  1.1e+03
# INSULIN   171.37 170.50  2.4e+03
# RESIST     97.78  92.00  2.1e+03
```

Check each variable, scatterplots, density estimates, QQ-Plots

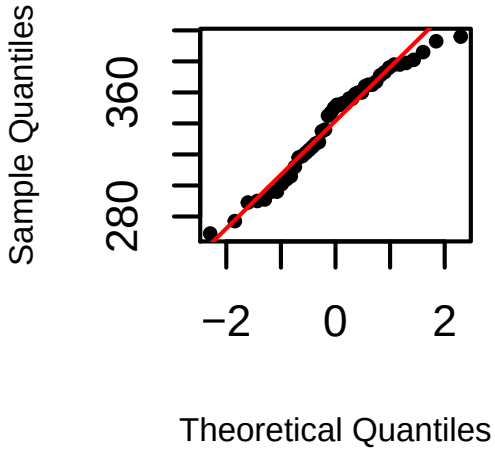
```
GGally::ggpairs(patients) # ggpairs() in package GGally

par(mfcol = c(2,3)) # 2x3 panel
for (p in 1:5){ # for loop qqplot for each variable
  qqnorm(patients[ , p],   # qqplot - normal
         main = paste(colnames(patients)[p]),
         cex = 0.8, cex.lab = 0.7, pch = 20)
  # use variable name as title
  qqline(patients[ , p], col = "red") # draw line
}
```


WEIGHT
FASTING
GLUCOSE
INSULIN
RESIST
Corr:
0.202
Corr:
0.186
Corr:
−0.0344
Corr:
0.372
Corr:
0.0939
Corr:
−0.0584
Corr:
−0.0537
Corr:
0.244
Corr:
0.0705
Corr:
0.507

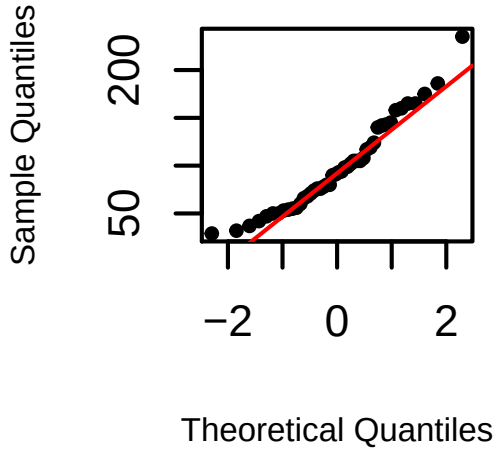
WEIGHT



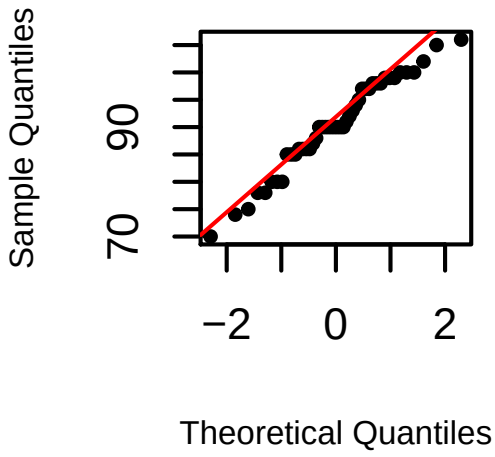
GLUCOSE



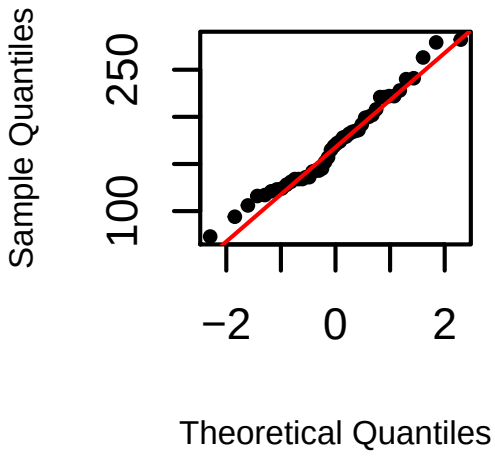
RESIST



FASTING



INSULIN



Univariate Normality Test

- The Kolmogorov-Smirnov (KS) test is used to decide if a sample comes from a population with a specific distribution.
  - test statistic does not depend on the underlying cumulative distribution function being tested (non-parametric)
  - exact test, not based on large-sample approximation
  - applies to continuous variables
  - tends to be more sensitive near the center of the distribution than at the tails.
- Null Hypothesis: The data follow a specified distribution

$$D = \max_{1 \leq i \leq n} \left(F(Y_i) - \frac{i-1}{n}, \frac{i}{n} - F(Y_i) \right)$$

- F is the theoretical CDF being tested (normal CDF if testing for normality)

Sample from Exponential Distribution, Skewed

```
x1 <- rexp(100) # sample from std. exponential dist'n
moments::skewness(x1) # skewed to the right
```

```
# [1] 1.7
```

```
ks.test(x1, "pnorm")
```

```
#
#   One-sample Kolmogorov-Smirnov test
#
# data:  x1
# D = 0.5, p-value <2e-16
# alternative hypothesis: two-sided
```

Sample from t-distribution, Symmetric, Heavy-Tails

```r
set.seed(21)
x2 <- rt(100, df = 3) # sample from t-dist with df = 3
moments::skewness(x2) # symmetric
```

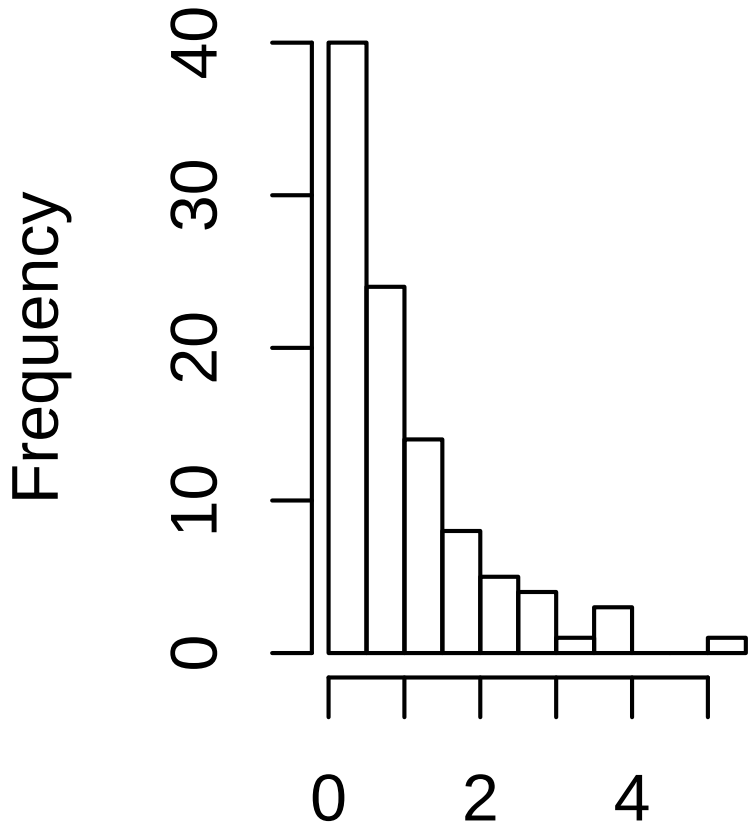
```
# [1] 1.6
```

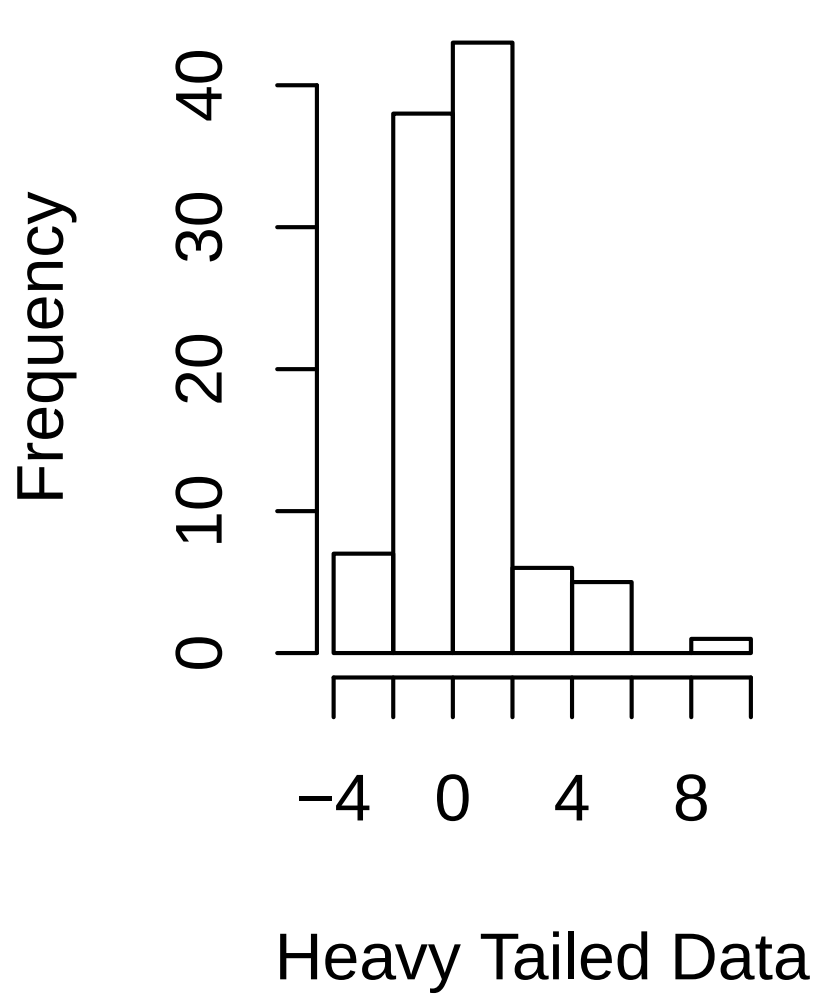
```r
ks.test(x2, "pnorm")
```

```
#
#   One-sample Kolmogorov-Smirnov test
#
# data:  x2
# D = 0.1, p-value = 0.2
# alternative hypothesis: two-sided
```

```r
# ks.test did not detect non-normality
```

```
par(mfcol = c(1,2))
hist(x1, xlab = "Skewed Data", main = "")
hist(x2, xlab = "Heavy Tailed Data", main = "")
```





Anderson-Darling Test

Anderson-Darling test is a KS-test variant which is sensitive to tail distribution variation/changes.

```
nortest::ad.test(x2) # need nortest package
```

```
#
#   Anderson-Darling normality test
#
# data:  x2
# A = 3, p-value = 2e-07
```

Reaven and Miller (1979) Data

```
tstat <- pval <- rep(NA, 5)
for(p in 1:5){
  test.out <- nortest::ad.test(patients[ , p])
  tstat[p] <- test.out$statistic
  pval[p] <- test.out$p.value
}
data.frame(variable = colnames(patients),
           AD.statistic = tstat, p.value = pval)
```

```
#   variable AD.statistic p.value
# 1   WEIGHT         0.52   0.179
# 2  FASTING         0.53   0.167
# 3  GLUCOSE         0.68   0.069
# 4  INSULIN         0.46   0.251
# 5   RESIST         0.68   0.070
```

Assessing Multivariate Normality - Chi-Square Plot

1. Compute the generalized squared (Mahalanobis) distance from each $\mathbf{X}_i$ to $\bar{\mathbf{X}}$ given by

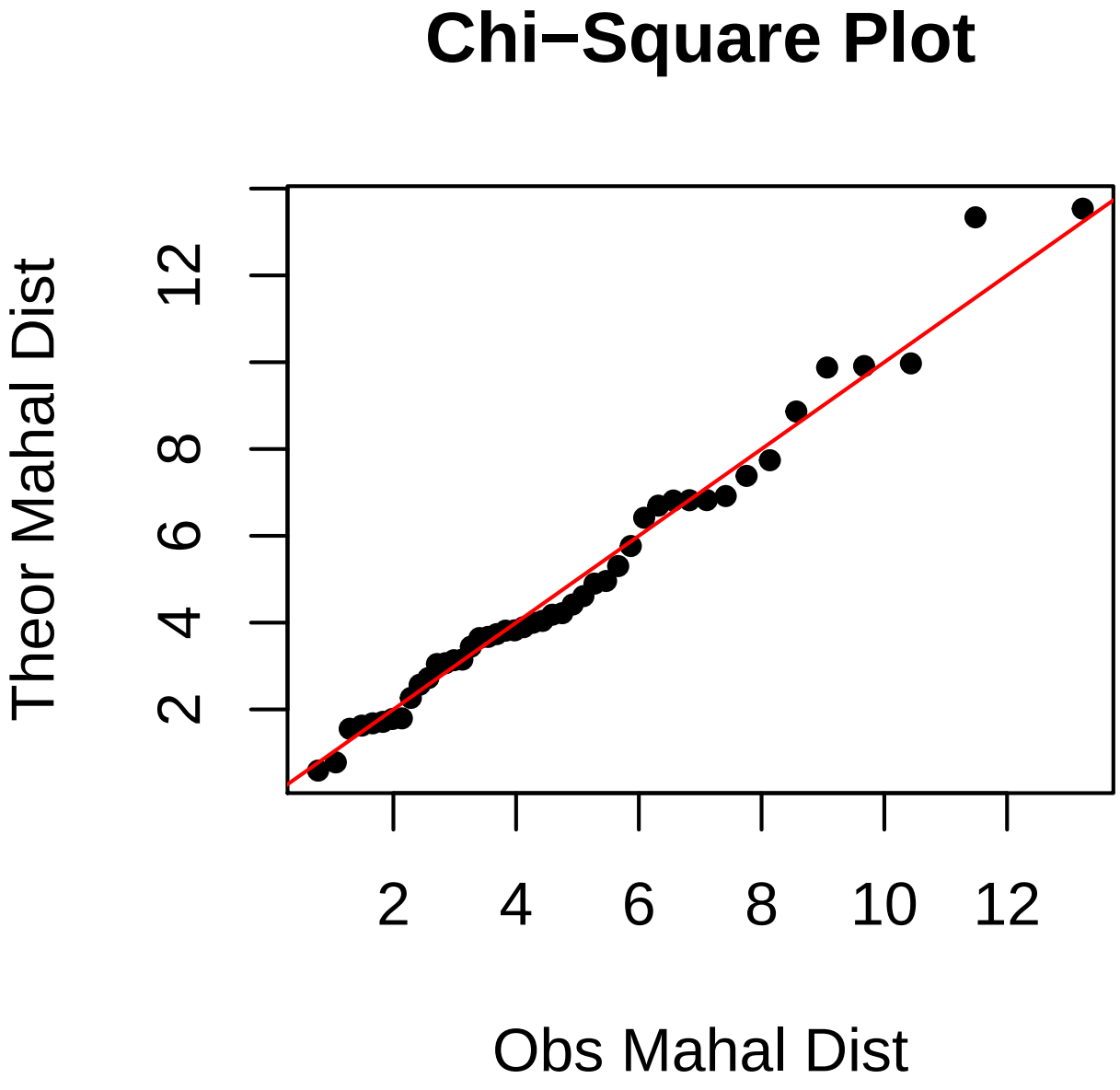
$$D_i^2 = (\mathbf{X}_i - \bar{\mathbf{X}})' \mathbf{S}^{-1} (\mathbf{X}_i - \bar{\mathbf{X}})$$

2. List D_i^2 from low to high. If $\mathbf{X}_i$ are multivariate normal, then D_i^2 has a Chi-Squared distribution.)
3. Form a $Q - Q$ plot based on the Chi-Squared distribution. \end{enumerate} If the line to a straight line, then it is reasonable to assume multivariate normal.

Chi-Square plots

```
ChiSq.plot <- function(data, main = "Chi-Square Plot"){
  # function for drawing chi-square plots
  x <- as.matrix(data)
  n <- nrow(data)
  xbar <- colMeans(data) # col means
  S <- var(data) # covariance matrix
  di2 <- rep(0,n) # storage for MD
  for (i in 1:n){     # MD distance for each observation
    di2[i] <- t(x[i,]-xbar) %*% solve(S) %*% (x[i,]-xbar)}
  CP.dat <- data.frame(expvals = qchisq((1:n)/(n+1),5) ,
                       obsvals = sort(di2))
  plot(CP.dat, pch =20, main = main, # plot the points
       xlab = "Obs Mahal Dist", ylab = "Theor Mahal Dist")
  lines(c(0,20), c(0,20), col="red")
}
```

```
ChiSq.plot(patients)
```



Multivariate Normal Goodness of Fit Test - Energy Test

The E-test of multivariate normality was proposed and implemented by Szekely and Rizzo (2005). The E-test of multivariate normality is implemented by parametric bootstrap with R replicates.

```
# mvnorm.etest() is in energy package
# R is number of bootstrap replicates
energy::mvnorm.etest(patients, R = 199)
```

```
#
#   Energy test of multivariate normality: estimated parame
#
# data:  x, sample size 46, dimension 5, replicates 199
# E-statistic = 1, p-value = 0.4
```

Radiation Levels Data

- The quality control department of a manufacturer of microwave ovens is required by the federal government to monitor the amount of radiation emitted when the doors of the ovens are closed.
- Observations of the radiation emitted through closed and open doors of $n = 42$ randomly selected ovens were made.

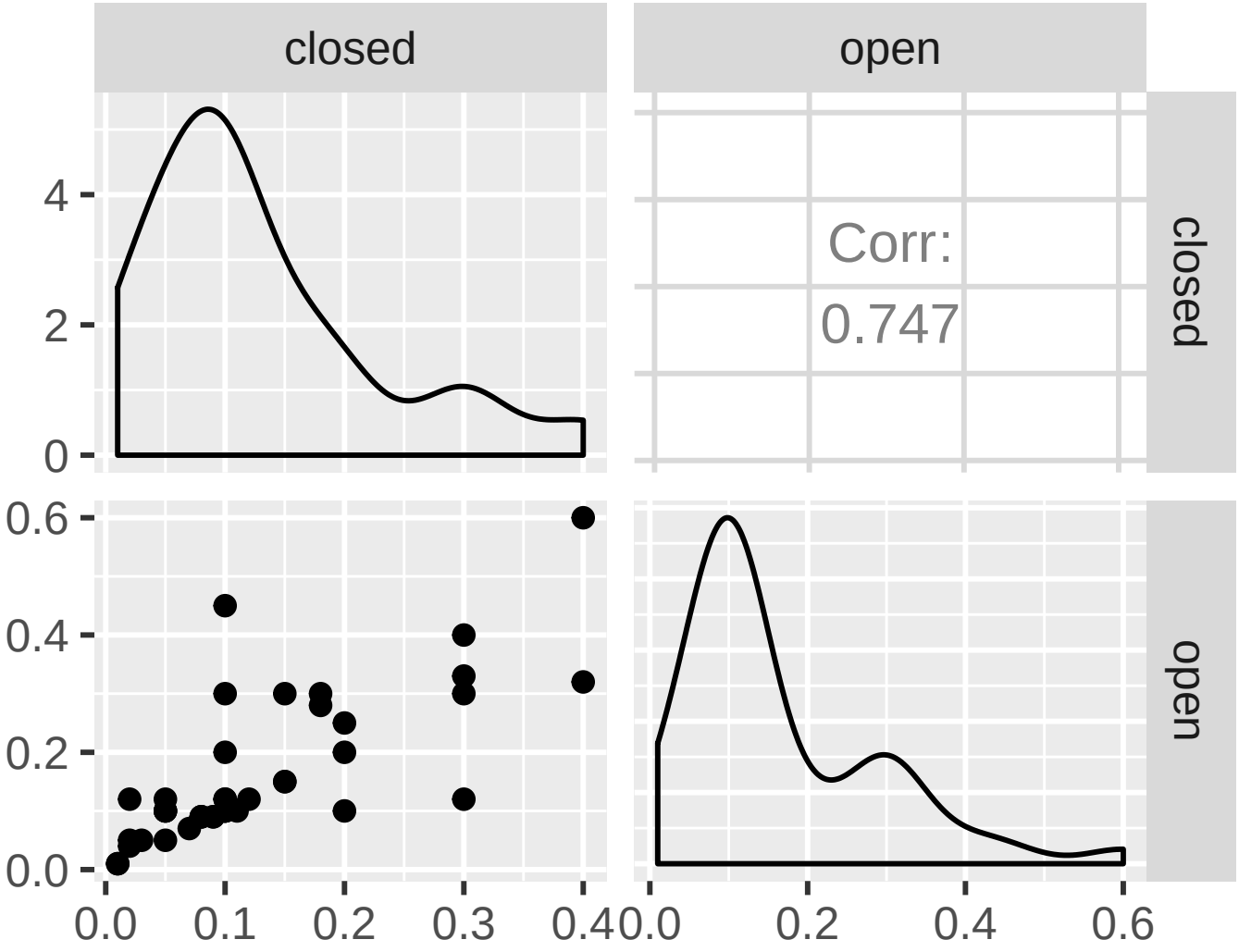
```
radiation <- read.table("radiation.txt", header = F)
colnames(radiation) <- c("closed","open")
moments::skewness(radiation)
```

```
# closed   open
#    1.2    1.5
```

```
# both variables are skewed to the right
```

Radiation Data Scatterplot

```
GGally::ggpairs(radiation)
```



Radiation Data, MVN Goodness of Fit Test

```
energy::mvnorm.etest(radiation, R = 500)
```

```
#
#   Energy test of multivariate normality: estimated parame
#
# data:  x, sample size 42, dimension 2, replicates 500
# E-statistic = 4, p-value <2e-16
```

Box-Cox Transformations

- A Box-Cox transformation of a variable x is defined as

$$x^{(\lambda)} = \begin{cases} \frac{x^{\lambda}-1}{\lambda} & \lambda \neq 0 \\ \ln x & \lambda = 0 \end{cases}$$

  which is continuous in λ for $x > 0$.
- These transformations are data based in the sense that it is only the appearance of the data that influences the choice of an appropriate transformation index by λ.
- Given observations $x_1, \ldots, x_n$, the Box-Cox solution for the choice of an appropriate power λ is the solution that maximizes the expression

$$\ell(\lambda) = -\frac{n}{2} \ln \left[\frac{1}{n} \sum_{j=1}^{n} (x_j^{(j)} - x^{(\bar{\lambda})})^2 \right] + (\lambda - 1) \sum_{j=1}^{n} \ln x_i$$

Box-Cox Transformations in R

```
library(car)
# compute appropriate power transformation
lam <- powerTransform(radiation)
summary(lam)
```

```
# bcPower Transformations to Multinormality
#        Est Power Rounded Pwr Wald Lwr bnd Wald Upr Bnd
# closed      0.16            0       -0.105          0.43
# open        0.15            0       -0.071          0.37
#
# Likelihood ratio tests about transformation parameters
#                             LRT df    pval
# LR test, lambda = (0 0)   2.3  2 3.1e-01
# LR test, lambda = (1 1) 51.1  2 7.9e-12
```

Transformed the Radiation Data

```
coef(lam)
```

```
# closed   open
#   0.16   0.15
```

```
radiation.transformed <- bcPower(with(radiation,
                      cbind(closed, open)), coef(lam))

moments::skewness(radiation.transformed) # skewness
```

```
# closed^0.16   open^0.15
#       -0.29       -0.30
```

Transformed Radiation Data Scatterplot

```
GGally::ggpairs(data.frame(radiation.transformed))
```